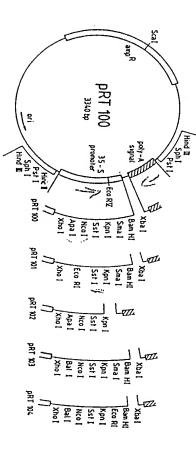
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optimal ribosome initiation in eukaryotes. (ACctcgagtggccaccatgg) well as the putative transcriptional start (--) and stop (-) are marked (ref.). Transcriptional fusions are possible with pRT101 containing Acctogagaaticgagite whereas pRT100, 102, 103, 104 lead to high expression of proteins initiated at into Smal of pRT103) the ATG codon is embedded in the consensus sequence for the respective ATG codon (Ncol site). In pRT103 and pRT104 (ccgaaticgg inserted CaMV sequences. TATA-box, ATG, and polyadenylation signal (underlined) as quence of pRT100 between its two Hindill sites is shown; capital letters indicate of CM 18411) were constructed in modified polylinkers of pUC18/192. The DNA sesignal of CaMV strain Cabb B-D (corresponding to bp 7016-7434 and 7436-7639 The plasmids pRT100-pRT104, carrying the 35S promoter and the polyadenylation



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a downstream inverted repeat underlined. replacing a reported Ser at residue 31 (no.27 in ref.1), (1v) extensive tetrapeptide with that deduced for the N-terminus of B.thuringiensis var kDa protein, in agreement with an estimated 43-kDa by gel electrophoresis -acid sequence of the B.sphaericus 2362 larvicidal toxin (1) were used to identify an EcoRI-HindIII fragment containing the entire coding sequence. Oligonucleotide probes designed on the basis of the known N-terminal 40 homology in the upstream control regions to B.t. subsp. kurstaki and israelensis (overlined). The putative Shine-Dalgarno sequence is boxed terminus which are not found in the purified toxin, (ii) homology of the (1). Features of note are (1) an additional four amino-acids at the N-Sequence analysis showed an ORF of 1110 nucleotides corresponding to a 41 israelensis and morrisoni (2), i.e. MRNI and MENI respectively, (111) Cys

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